














Sequences producing significant alignments:			Score (bits)	E Value	
<u>gi 21536376 ref NP_005493.2 </u>	ATP-binding cassette, sub-fami...	<u>657</u>	0.0		
<u>gi 13876613 gb AAK43526.1 </u>	ATP-binding cassette 1 sub-famil...	<u>657</u>	0.0		
<u>gi 5734135 gb AAD49852.1 </u>	ATP cassette binding transporter ...	<u>657</u>	0.0		
<u>gi 9755159 gb AAF98175.1 </u>	ATP-binding cassette transporter ...	<u>657</u>	0.0		
<u>gi 13123945 sp O95477 ABC1_HUMAN</u>	ATP-binding cassette, sub-...	<u>647</u>	0.0		
<u>gi 4128033 emb CAA10005.1 </u>	ATP-binding cassette transporter...	<u>647</u>	0.0		
<u>gi 9247086 gb AAF86276.1 </u>	ABCA1 [Homo sapiens]	<u>646</u>	0.0		
<u>gi 13124694 sp P41233 ABC1_MOUSE</u>	ATP-binding cassette, sub-...	<u>593</u>	e-168		
<u>gi 1082238 pir A54774</u>	ATP binding cassette transporter ABC...	<u>593</u>	e-168		
<u>gi 11611825 gb AAG39073.1 </u>	ATP-binding cassette 1, sub-fami...	<u>593</u>	e-168		
<u>gi 34577069 ref NP_038482.2 </u>	ATP-binding cassette 1, sub-fa...	<u>593</u>	e-168		
<u>gi 30017417 ref NP_835196.1 </u>	ATP-binding cassette, sub-fami...	<u>587</u>	e-166		
<u>gi 45383826 ref NP_989476.1 </u>	ATP-binding cassette, sub-fami...	<u>476</u>	e-133		
<u>gi 47220000 emb CAG11533.1 </u>	unnamed protein product [Tetrao...	<u>304</u>	2e-81		
<u>gi 47212013 emb CAF95419.1 </u>	unnamed protein product [Tetrao...	<u>300</u>	4e-80		

gi 47211165 emb CAF95992.1 	unnamed protein product [Tetrao...	264	4e-69	
gi 27806343 ref NP_776646.1 	ATP-binding cassette, sub-fami...	185	1e-45	L
gi 34859941 ref XP_241525.2 	similar to ATP-binding cassett...	183	5e-45	L
gi 6671495 ref NP_031404.1 	ATP-binding cassette, sub-famil...	179	1e-43	L
gi 47219577 emb CAG02283.1 	unnamed protein product [Tetrao...	169	1e-40	
gi 2959643 qb AAC05632.1 	rim ABC transporter [Homo sapiens]	149	9e-35	L
gi 6707663 sp P78363 ABCR_HUMAN	Retinal-specific ATP-bindin...	148	2e-34	L
gi 4557876 ref NP_000341.1 	ATP-binding cassette, sub-famil...	148	2e-34	L
gi 2969966 emb CAA75729.1 	ABCR [Homo sapiens]	148	2e-34	L
gi 3243082 qb AAC23915.1 	ATP-binding cassette transporter ...	148	2e-34	L
gi 40556959 qb AAR87836.1 	ABCA4 [Canis familiaris]	147	4e-34	
gi 40556955 qb AAR87834.1 	ABCA4 [Canis familiaris]	147	4e-34	
gi 40556957 qb AAR87835.1 	ABCA4 [Canis familiaris]	147	4e-34	
gi 47223059 emb CAG07146.1 	unnamed protein product [Tetrao...	132	1e-29	
gi 47225166 emb CAF98793.1 	unnamed protein product [Tetrao...	131	3e-29	
gi 34862327 ref XP_216829.2 	similar to ATP-binding cassett...	127	4e-28	L
gi 46485412 ref NP_997481.1 	ATP-binding cassette, sub-fami...	127	4e-28	L
gi 15451840 ref NP_038878.1 	ATP-binding cassette, sub-fami...	127	7e-28	L
gi 15451838 ref NP_150651.1 	ATP-binding cassette, sub-fami...	98	5e-19	L
gi 9506365 ref NP_061985.1 	ATP-binding cassette, sub-famil...	98	5e-19	L
gi 22725156 qb AAN04657.1 	ABC transporter ABCA7 [Homo sapi...	98	5e-19	L
gi 12656651 qb AAK00959.1 	ABC transporter member 7 [Homo s...	98	5e-19	L
gi 46139435 ref XP_391408.1 	hypothetical protein FG11232.1...	36	1.5	
gi 45446740 ref NP_001597.2 	ATP-binding cassette, sub-fami...	35	2.7	L
gi 1082239 pir B54774	ATP binding cassette transporter ABC...	35	2.7	
gi 47078218 ref NP_997698.1 	ATP-binding cassette, sub-fami...	35	2.7	L
gi 9957467 qb AAG09372.1 	ATP-binding cassette sub-family A...	35	2.7	L
gi 11346269 pir A59189	ATP-binding cassette transporter - ...	35	2.7	
gi 11993939 ref NP_031405.1 	ATP-binding cassette, sub-fami...	35	2.7	L
gi 14916523 sp Q9BZC7 ABC2_HUMAN	ATP-binding cassette, sub-...	35	2.7	L
gi 13242308 ref NP_077372.1 	ATP-binding cassette, sub-fami...	35	2.7	L
gi 47209044 emb CAF91746.1 	unnamed protein product [Tetrao...	35	3.6	
gi 14250599 qb AAH08755.1 	ABCA2 protein [Homo sapiens]	35	3.6	L
gi 47212140 emb CAF95654.1 	unnamed protein product [Tetrao...	34	8.7	
gi 42491191 emb CAF25489.1 	HuvD protein [Listonella anguil...	34	8.7	
gi 13475669 ref NP_107236.1 	3-hydroxybutyryl-coA dehydroge...	33	12	
gi 48846428 ref ZP_00300691.1 	COG1283: Na+/phosphate sympo...	33	16	
gi 21430570 qb AAM50963.1 	RE06730p [Drosophila melanogaster]	33	16	L
gi 33519597 ref NP_878429.1 	carbamoyl-phosphate synthase l...	33	16	
gi 24648559 ref NP_650925.1 	CG3822-PA [Drosophila melanoga...	33	16	L
gi 50294708 ref XP_449765.1 	unnamed protein product [Candi...	33	16	
gi 47215635 emb CAG01352.1 	unnamed protein product [Tetrao...	32	21	
gi 2631999 emb CAA05373.1 	MviN protein [Vibrio cholerae]	32	28	
gi 15640699 ref NP_230329.1 	MviN protein [Vibrio cholerae ...	32	28	
gi 21428506 qb AAM49913.1 	LD28992p [Drosophila melanogaster]	32	28	L
gi 28379892 ref NP_786784.1 	ATP-dependent Clp protease, AT...	32	28	
gi 48102288 ref XP_395322.1 	similar to CG3999-PA [Apis mel...	32	28	L
gi 39583220 emb CAE61438.1 	Hypothetical protein CBG05321 [...	32	28	
gi 49072300 ref XP_400439.1 	hypothetical protein UM02824.1...	32	28	
gi 23577904 ref NP_703103.1 	unknown [Rachiplusia ou multip...	32	28	
gi 16769402 qb AAL28920.1 	LD29423p [Drosophila melanogaster]	32	28	L

gi 24639632 ref NP_572152.2	CG4857-PB [Drosophila melanoga...	32	28	L
gi 28897306 ref NP_796911.1	MviN protein [Vibrio parahaemo...	32	28	
gi 32405532 ref XP_323379.1	predicted protein [Neurospora ...	32	28	
gi 4185888 emb CAA21827.1	EG:EG0007.4 [Drosophila melanoga...	32	28	
gi 50290817 ref XP_447841.1	unnamed protein product [Candi...	32	28	
gi 22788744 ref NP_690455.1	DNA ligase III [Heliothis zea ...	32	28	
gi 15894929 ref NP_348278.1	Aspartate ammonia-lyase [Clostr...	32	38	
gi 46121537 ref XP_385323.1	hypothetical protein FG05147.1...	32	38	
gi 48104558 ref XP_395803.1	similar to ENSANGP00000016433 ...	32	38	L
gi 20806867 ref NP_622038.1	ABC-type dipeptide/oligopeptid...	31	51	
gi 16765904 ref NP_461519.1	leucine-rich repeat protein [P...	31	51	
gi 45361665 ref NP_989410.1	hypothetical protein MGC76219 ...	31	51	L
gi 39996841 ref NP_952792.1	Na/Pi-cotransporter family pro...	31	51	
gi 39998079 ref NP_954030.1	conserved hypothetical protein...	31	51	
gi 9049789 gb AAF82481.1	leucine-rich repeat protein [phag...	31	51	
gi 21243605 ref NP_643187.1	conserved hypothetical protein...	31	51	
gi 41408181 ref NP_961017.1	hypothetical protein MAP2083c ...	31	51	
gi 49903552 gb AAH76991.1	MGC76219 protein [Xenopus tropic...	31	51	L
gi 34896534 ref NP_909611.1	putative retrotransposon gag p...	31	51	
gi 31544841 ref NP_853419.1	ATP/GTPase [Mycoplasma gallise...	31	68	
gi 37181847 gb AAQ88727.1	JAM-IT/VE-JAM [Homo sapiens]	31	68	
gi 10864029 ref NP_067042.1	junctional adhesion molecule 2...	31	68	L
gi 7109693 gb AAF36764.1	putative ATP/GTP-binding protein ...	31	68	
gi 39590633 emb CAE65003.1	Hypothetical protein CBG09841 [...	31	68	
gi 2492605 sp P97998 MDL1 CANAL	ATP-dependent permease MDL1...	31	68	
gi 19110396 gb AAL82538.1	C21ORF43 [Homo sapiens]	31	68	L
gi 46440040 gb EAK99351.1	hypothetical protein CaO19.2615 ...	31	68	
gi 39594406 emb CAE71984.1	Hypothetical protein CBG19059 [...	31	68	
gi 6635285 gb AAF19761.1	mutant matrix melanosomal protein...	30	91	L
gi 38076905 ref XP_127911.3	RIKEN cDNA 2410089E03 [Mus mus...	30	91	L
gi 39580881 emb CAE73879.1	Hypothetical protein CBG21472 [...	30	91	
gi 38346799 emb CAD41367.2	OSJNBa0088A01.6 [Oryza sativa (...	30	91	
gi 34862223 ref XP_343147.1	similar to Melanocyte protein ...	30	91	L
gi 49255967 gb AAH71083.1	Unknown (protein for IMAGE:63160...	30	91	

Alignments

☐ >gi|21536376|ref|NP_005493.2| **L** ATP-binding cassette, sub-family A member 1; ATP
 high density lipoprotein deficiency, Tangier type, 1;
 cholesterol efflux regulatory protein [Homo sapiens]
 Length = 2261

Score = 657 bits (1543), Expect = 0.0

Identities = 237/286 (82%), Positives = 240/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELELQPW EQYTFVSNDAPEDTGTLELLNALT PGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELELQPWYNEQYTFVSNDAPEDTGTLELLNALT KDPPGFGTRCMEGNPIPDTPCQ 1430
 Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPS PACQCSSD--UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPS PACQCSSD KKMLPVCPPGAGGLPPPQ

Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 115 QNTADILQDLTGM-ISDYLVK TW-QIIAKSLU-----MNEFRYGGFSLGVSNTQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPSQE

Sbjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1550

Query: 169 -GDAIKQM-UHL-----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV

Sbjct: 1551 VNDAIKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTKNNVKVWFNNKGWHAISSFLNV 1608

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD

Sbjct: 1609 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

☐ >[gi|13876613|gb|AAK43526.1|](#) ☒ ATP-binding cassette 1 sub-family A member 1 [Homo
 Length = 2261

Score = 657 bits (1543), Expect = 0.0
 Identities = 237/286 (82%), Positives = 240/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSLELQPW--UEQYTFVSNDAPE DTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSLELQPW EQYTFVSNDAPE DTGTLELLNALT PGFGTRCMEGNPIPDTPCQ

Sbjct: 1371 FGKYPSLELQPW MYNEQYTFVSNDAPE DTGTLELLNALT KD PGFGTRCMEGNPIPDTPCQ 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD KKMLPVCPPGAGGLPPPQ

Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 115 QNTADILQDLTGM-ISDYLVK TW-QIIAKSLU-----MNEFRYGGFSLGVSNTQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPSQE

Sbjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1550

Query: 169 -GDAIKQM-UHL-----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV

Sbjct: 1551 VNDAIKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNV 1608

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD

Sbjct: 1609 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

☐ >[gi|5734135|gb|AAD49852.1|](#) ☒ ATP cassette binding transporter 1 [Homo sapiens]
 Length = 849

Score = 657 bits (1543), Expect = 0.0
 Identities = 237/286 (82%), Positives = 240/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSLELQPW--UEQYTFVSNDAPE DTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSLELQPW EQYTFVSNDAPE DTGTLELLNALT PGFGTRCMEGNPIPDTPCQ

Sbjct: 428 FGKYPSLELQPW MYNEQYTFVSNDAPE DTGTLELLNALT KD PGFGTRCMEGNPIPDTPCQ 487

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD KKMLPVCPPGAGGLPPPQ

Sbjct: 488 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 547

Query: 115 QNTADILQDLTGM-ISDYLVK TW-QIIAKSLU-----MNEFRYGGFSLGVSNTQALPPSQE 168

QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPSQE
 Sbjct: 548 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 607

Query: 169 -GDAIKQM-UHL-----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV
 Sbjct: 608 VNDAIKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTKNNVKVWFNNKGWHAISSFLNV 665

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 666 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 711

☐ >gi|9755159|gb|AAF98175.1| ☒ ATP-binding cassette transporter 1 [Homo sapiens]
 Length = 2261

Score = 657 bits (1543), Expect = 0.0
 Identities = 237/286 (82%), Positives = 240/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSLELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSLELQPW EQYTFVSNDAPEDTGTLELLNALT PGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSLELQPWMYNEQYTFVSNDAPEDTGTLELLNALT KD PGFGTRCMEGNPIPDTPCQ 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD KIKKMLPVCPPGAGGLPPPQRK 1490

Query: 115 QNTADILQDLTG-ISDYLVKTW-QIIAKSLU----MNEFRYGGFSLGVSNTQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPSQE
 Sbjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1550

Query: 169 -GDAIKQM-UHL-----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV
 Sbjct: 1551 VNDAIKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNV 1608

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1609 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

☐ >gi|13123945|sp|O95477|ABC1_HUMAN ☒ ATP-binding cassette, sub-family A, member 1
 transporter 1) (ATP-binding cassette 1) (ABC-1)
 (Cholesterol efflux regulatory protein)
 Length = 2261

Score = 647 bits (1519), Expect = 0.0
 Identities = 235/286 (82%), Positives = 238/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSLELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSLELQPW EQYTFVSNDAPEDTGTLELLNALT PGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSLELQPWMYNEQYTFVSNDAPEDTGTLELLNALT KD PGFGTRCMEGNPIPDTPCQ 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD KIKKMLPVCPPGAGGLPPPQRK 1490

Query: 115 QNTADILQDLTG-ISDYLVKTW-QIIAKSLU----MNEFRYGGFSLGVSNTQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPSQE

Sbjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1550

Query: 169 -GDAIKQM-UHL-----CASSAD--LNSLGT-MTGLDT---YKV---UKG--AISSFLNV 210
 DA KQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV

Sbjct: 1551 VNDATKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNV 1608

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVA MTTSVD

Sbjct: 1609 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVD 1654

☐ >gi|4128033|emb|CAA10005.1| ☒ ATP-binding cassette transporter-1 (ABC-1) [Homo s
 gi|5734101|gb|AAD49849.1| ☒ ATP cassette binding transporter 1 [Homo sapiens]
 Length = 2201

Score = 647 bits (1519), Expect = 0.0
 Identities = 235/286 (82%), Positives = 238/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSLELQPW--UEQYTFVSNDAPEdTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSLELQPW EQYTFVSNDAPEdTGTLELLNALT PGFGTRCMEGNPIPDTPCQ

Sbjct: 1311 FGKYPSLELQPWMYNEQYTFVSNDAPEdTGTLELLNALT KD PGFGTRCMEGNPIPDTPCQ 1370

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD KKMLPVCPPGAGGLPPPQ

Sbjct: 1371 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD KIKMLPVCPPGAGGLPPPQRK 1430

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU----MNEFRYGGFSLGVSNTQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPSQE

Sbjct: 1431 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1490

Query: 169 -GDAIKQM-UHL-----CASSAD--LNSLGT-MTGLDT---YKV---UKG--AISSFLNV 210
 DA KQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV

Sbjct: 1491 VNDATKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNV 1548

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVA MTTSVD

Sbjct: 1549 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVD 1594

☐ >gi|9247086|gb|AAF86276.1| ☒ ABCA1 [Homo sapiens]
 Length = 2261

Score = 646 bits (1517), Expect = 0.0
 Identities = 235/286 (82%), Positives = 238/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSLELQPW--UEQYTFVSNDAPEdTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSLELQPW EQYTFVSNDAPEdTGTLELLNALT PGFGTRCMEGNPIPDTPCQ

Sbjct: 1371 FGKYPSLELQPWMYNEQYTFVSNDAPEdTGTLELLNALT KD PGFGTRCMEGNPIPDTPCQ 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD KKMLPVCPPGAGGLPPPQ

Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD KIKMLPVCPPGAGGLPPPQRK 1490

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU----MNEFRYGGFSLGVSNTQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPSQE

Sbjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1550

Query: 169 -GDAIKQM-UHL-----CASSAD--LNSLGT-MTGLDT---YKV---UKG--AISSFLNV 210
 DA KQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV
 Sbjct: 1551 VNDAXKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNV 1608

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVA MTTSVD
 Sbjct: 1609 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAXMTTSVD 1654

☐ >[gi|13124694|sp|P41233|ABC1_MOUSE](#) ☒ ATP-binding cassette, sub-family A, member 1
 transporter 1) (ATP-binding cassette 1) (ABC-1)
 Length = 2261

Score = 593 bits (1391), Expect = e-168
 Identities = 219/286 (76%), Positives = 231/286 (80%), Gaps = 35/286 (12%)

Query: 1 FGKYPSLELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSLELQPW EQYTFVSNDAPEDTGTLELLNALT PGFGTRCMEGNPIPDTPC
 Sbjct: 1371 FGKYPSLELQPWYNEQYTFVSNDAPEDMGTQELNALT KD PGFGTRCMEGNPIPDTPCL 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMKNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEE+WT +PVPQ+I+DLFQNGNWTM+NPSPACQCSSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1431 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU----MNEFRYGGFSLGVSNTQALPPSQE 168
 Q TADILQ+LTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPS E
 Sbjct: 1491 QKTADILQNL TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSHE 1550

Query: 169 -GDAIKQMUHL-----CASSAD--LNSLGT-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM L +SAD L+SLG M GLDT KV KG AISSFLNV
 Sbjct: 1551 VNDAIKQMKKLLKLTKD--TSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNV 1608

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1609 INNAILRANLQKGENPSYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

☐ >[gi|1082238|pir||A54774](#) ATP binding cassette transporter ABC1 - mouse
[gi|495257|emb|CAA53530.1|](#) ☒ ABC transporter [Mus musculus]
 Length = 2201

Score = 593 bits (1391), Expect = e-168
 Identities = 219/286 (76%), Positives = 231/286 (80%), Gaps = 35/286 (12%)

Query: 1 FGKYPSLELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSLELQPW EQYTFVSNDAPEDTGTLELLNALT PGFGTRCMEGNPIPDTPC
 Sbjct: 1311 FGKYPSLELQPWYNEQYTFVSNDAPEDMGTQELNALT KD PGFGTRCMEGNPIPDTPCL 1370

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMKNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEE+WT +PVPQ+I+DLFQNGNWTM+NPSPACQCSSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1371 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1430

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU----MNEFRYGGFSLGVSNTQALPPSQE 168
 Q TADILQ+LTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPS E
 Sbjct: 1431 QKTADILQNL TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSHE 1490

Query: 169 -GDAIKQMUHL-----CASSAD--LNSLGT-MTGLDT---YKV---UKG--AISSFLNV 210

DAIKQM L +SAD L+SLG M GLDT KV KG AISSFLNV
 Sbjct: 1491 VNDAIKQMKLLKLT KD--TSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNV 1548

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1549 INNAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1594

☐ >gi|11611825|gb|AAG39073.1| ☒ ATP-binding cassette 1, sub-family A, member 1 [Mu]
 Length = 2198

Score = 593 bits (1391), Expect = e-168
 Identities = 219/285 (76%), Positives = 230/285 (80%), Gaps = 35/285 (12%)

Query: 1 FGKYPSLELQPW--UEQYTFVSNDAPE DTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSLELQPW EQYTFVSNDAPE DTGTLELLNALT PGFGTRCMEGNPIPDTPC
 Sbjct: 1311 FGKYPSLELQPW MYNEQYTFVSNDAPE DMGTQELLNALT KD PGFGTRCMEGNPIPDTPCL 1370

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD--UKKMLPVCPPGAGGLPPPQ-M 114
 AGEE+WT +PVPQ+I+DLFQNGNWTM+NPSPACQCSSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1371 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1430

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU----MNEFRYGGFSLGVSNTQALPPSQE 168
 Q TADILQ+LTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPS E
 Sbjct: 1431 QKTADILQNL TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSHE 1490

Query: 169 -GDAIKQMUHL-----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 211
 DAIKQM L SAD L+SLG M GLDT KV KG AISSFLNV+
 Sbjct: 1491 VNDAIKQMKLLKLT KD---SADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVI 1547

Query: 212 --AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 AIL NLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1548 NNAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1592

☐ >gi|34577069|ref|NP_038482.2| ☒ ATP-binding cassette 1, sub-family A, member 1;
 1 [Mus musculus]
 Length = 2261

Score = 593 bits (1391), Expect = e-168
 Identities = 219/286 (76%), Positives = 231/286 (80%), Gaps = 35/286 (12%)

Query: 1 FGKYPSLELQPW--UEQYTFVSNDAPE DTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSLELQPW EQYTFVSNDAPE DTGTLELLNALT PGFGTRCMEGNPIPDTPC
 Sbjct: 1371 FGKYPSLELQPW MYNEQYTFVSNDAPE DMGTQELLNALT KD PGFGTRCMEGNPIPDTPCL 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD--UKKMLPVCPPGAGGLPPPQ-M 114
 AGEE+WT +PVPQ+I+DLFQNGNWTM+NPSPACQCSSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1431 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU----MNEFRYGGFSLGVSNTQALPPSQE 168
 Q TADILQ+LTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPS E
 Sbjct: 1491 QKTADILQNL TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSHE 1550

Query: 169 -GDAIKQMUHL-----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM L +SAD L+SLG M GLDT KV KG AISSFLNV
 Sbjct: 1551 VNDAIKQMKLLKLT KD---TSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNV 1608

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1609 INNAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

☐ >gi|30017417|ref|NP_835196.1| ☒ ATP-binding cassette, sub-family A (ABC1), membe
 norvegicus]
 gi|28912192|gb|AA053557.1| ☒ ATP-binding cassette 1 [Rattus norvegicus]
 Length = 2201

Score = 587 bits (1378), Expect = e-166
 Identities = 217/286 (75%), Positives = 231/286 (80%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELELQPW--UEQYTFVSNDAPE DTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYP+LELQPW EQYTFVSNDAPE GT ELLNALT PGFGTRCMEGNPIP+TPC
 Sbjct: 1311 FGKYPNLELQPWMYNEQYTFVSNDAPE DMGTQELLNALT KD PGFGTRCMEGNPIPNTPC 1370

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSD--UKKMLPVCPPGAGGLPPPQ-M 114
 GEE+WTT PVPQT+MDLFQNGNWTM+NPSP+CQCSSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1371 VGEEDWTTGPVPQTLMDLFQNGNWTMKNPSPSCQCSSDKIKKMLPVCPPGAGGLPPPQRK 1430

Query: 115 QNTADILQDLTGM-ISDYLVK TW-QIIAKSLU-----MNEFRYGGFSLGVSNTQALPPSQE 168
 Q TADILQ+LTG SDYLVKT+ QIIAKSL +NEFRYGGFSLGVS++QALPPSQE
 Sbjct: 1431 QKTADILQNL TGRNNSDYLVKTYVQIIAKSLKNKVWVNEFRYGGFSLGVS D SQALPPSQE 1490

Query: 169 -GDAIKQMUHL-----CASSAD--LNSL GU-MTGLDT---YKV---UKG--AISSFLNV 210
 +AIKQM L SSAD L+SLG MTGLDT KV KG AISSFLNV
 Sbjct: 1491 VNNAIKQMKKLLKLT KD--SSAD RFLSSLGRFMTGLDTKNNVKVWFNNKGWHAISSFLNV 1548

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1549 INNAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1594

☐ >gi|45383826|ref|NP_989476.1| ☒ ATP-binding cassette, sub-family A (ABC1), membe
 gi|18028983|gb|AAL56247.1| ☒ ATP-binding cassette transporter 1 [Gallus gallus]
 Length = 2260

Score = 476 bits (1115), Expect = e-133
 Identities = 187/286 (65%), Positives = 218/286 (76%), Gaps = 36/286 (12%)

Query: 1 FGKYPSELELQPWU--EQYTFVSNDAPE DTGTLELLNALT--TPGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELELQPW EQYTF+SNDAPE GT +LL+AL PGFGTRCM+G+ IPDTPC
 Sbjct: 1371 FGKYPSELELQPWYDEQYTFISNDAPE D AGTQKLLDALLNKPGFGTRCMQGH SIPDT PCT 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDU--KKMLPVCPPGAGGLPPPQM- 114
 G++EWTTA VP +++++ + GNW+M+NPSP+C+CS++ KKMLPVCPPGAGGLPPPQ
 Sbjct: 1431 VGQKEWTTASVPDSVLEILR-GNWSMENPSPSCECSNEKIKKMLPVCPPGAGGLPPPQRE 1489

Query: 115 QNTADILQDLTGM-ISDYLVK TW-QIIAKSLU-----MNEFRYGGFSLGVSNTQALPPSQE 168
 Q+TADILQ+LTG ISDYLVKT+ QII KSL +NEFRYGGFSLG ++ LPPS E
 Sbjct: 1490 QDTADILQNL TGRNISDYLVKTYAQIIGKSLKNKIWVNEFRYGGFSLGARSSHVLPSSNE 1549

Query: 169 G-DAIKQ-----MUHL CASSAD--LNSL GU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQ + SS D LN+L M GLDT KV KG AI+SFLNV
 Sbjct: 1550 VTDAIKQVKKILELAQ--GSSGDRFLNNLASFMKGLDTKNNVKVWFNNKGWHAIASFLNV 1607

=> FIL HOME		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.06	0.27

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=> FILE .RECEPTOR		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.48

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 L2 42 DUP REM L1 (42 DUPLICATES REMOVED)

=> S L2 AND GLYBURIDE
 L3 1 L2 AND GLYBURIDE

=> D L3

L3 ANSWER 1 OF 1 MEDLINE on STN
 AN 2002348480 MEDLINE
 DN PubMed ID: 12091489
 TI LXR/RXR activation enhances basolateral efflux of cholesterol in CaCo-2 cells.
 AU Murthy Shubha; Born Ella; Mathur Satya N; Field F Jeffrey
 CS Department of Veterans Affairs and Department of Internal Medicine, University of Iowa, Iowa City, IA 52242, USA.. shubha-murthy@uiowa.edu
 NC HL49264 (NHLBI)
 SO Journal of lipid research, (2002 Jul) 43 (7) 1054-64.
 Journal code: 0376606. ISSN: 0022-2275.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 200212
 ED Entered STN: 20020702
 Last Updated on STN: 20030204
 Entered Medline: 20021220

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